

A report on the Research Article titled "SEIR model for COVID-19 dynamics incorporating the environment and social distancing" by *Samuel Mwalili, Mark Kimathil, Viona Ojiambo, Duncan Gathungu, and Rachel Mbogo*

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Abstract

The goal of this report on the given paper was to apply a modified susceptible exposed infectious recovered (SEIR) compartmental mathematical model for the prediction of COVID-19 epidemic dynamics incorporating pathogens in the environment and interventions. This report is mainly focused on social distancing in India, and how it varied during the second outbreak of the COVID-19 quarantine period. The given model shows, the epidemic rate from humans and pathogens to hosts, and in the extended model the same method is followed for different data. In this report, we analyzed the given data using a compartmental model, the next-generation matrix approach was used to determine the basic reproduction number R_0 . The model equations are solved numerically using fourth and fifth-order Runge–Kutta methods, and also calculated disease-free-equilibrium point (DFE).

Results of a given model: The authors found in their model an R_0 of 2.03, implying that the pandemic will persist in the human population in the absence of strong control measures. Results after simulating various scenarios indicate that disregarding social distancing and hygiene measures can have devastating effects on the human population. The model shows that quarantine of contacts and isolation of cases can help halt the spread of novel coronavirus.

Results of an extended model: We found an R_0 of 0.56 in the extended model, suggesting that the epidemic can be halted when people follow social distancing and good hygiene.

Keywords: SEIRP model, Social distancing, Compartmental model, Basic reproduction number, Next-generation matrix, COVID-19 dynamics, Simulation.

Background

On December 31, 2019, China notified the World Health Organization (WHO) about pneumonia patients with an unknown cause that had been found in Wuhan, Hubei province while cautioning against travel or commercial delays to and from China. China's national authorities reported to the WHO a total of 44 people with pneumonia of unknown cause from December 31, 2019, to January 3, 2020. The Huanan Seafood Wholesale Market had previously been linked to the instances that were initially discovered. Fever (98.6 % of early clinical cases), tiredness (69.6 %), and dry cough (59.4 %) were the most prevalent clinical traits in Wuhan, China [2].

The first occurrence in Germany was officially confirmed on January 27, 2020, close to Munich. The first two verified COVID-19-related deaths occurred on March 9, 2020, in Essen and Heinsberg. The WHO formally declared COVID-19 a worldwide pandemic on March 11, 2020, which denotes a disease that has spread across the globe. Borders with Austria, Denmark, France, Luxembourg, and Switzerland were blocked on March 15, 2020, and curfews were imposed. As of 20 weeks after the initial incidence, around 80 percent of reported cases in Germany exhibit mild to moderate symptoms. By April 17, 2020, the Koch Institute reported that there have been around 130,000 infection-confirmed cases and 4000 COVID-19-related fatalities in Germany. The risk of the COVID-19 pandemic for the population in Germany was initially rated by the Robert Koch Institute (RKI), the government's principal scientific institution in the field of bio-medicine, as "low to moderate" on February 28, 2020, then as "high" on March 17 and "very high" on March 26—especially for risk groups [6].

The first case of COVID-19 infection in India was discovered in Kerala. A 20-year-old woman with a sore throat and dry cough who had only been experiencing them for one day brought herself to the emergency room of the general hospital in Thrissur, Kerala, on January 27, 2020. No prior history of fever, rhinitis, or shortness of breath was present [14].

Introduction

The new virus was designated COVID-19, where CO stands for corona, VID stands for a viral disease, and 19 stands for the year of the outbreak. A Chinese scientist confirmed the virus can be conveyed from person to person on January 21, 2020. WHO issued a public health emergency on January 31, 2020. Real-time RT-PCR was used to confirm cases, and epidemiological, demographic, clinical, and radiological aspects, as well as laboratory data, were examined. The results were tracked until January 25, 2020.

In estimating the situation of the epidemic we can use the Mathematical model for checking the social distancing in various places. Here we use different parameters and R_0 . The primary reproduction number, abbreviated R_0 , is an important aspect in the mathematical modeling of any disease. It's also referred to as the primary reproduction ratio. If R_0 is equal to 1, the outbreak is assumed to be spreading, and if R_0 is less than 1, it is assumed to be over. $R(t)$ is a reproduction number that varies with time. In this research article, we will estimate the reproduction number and we will create our own model in the extension of a given model. We will use the data from India and simulate it along with the suitable parameters. Moreover, we will compare our results with the author's results. Finally, We will provide some limitations, possible extensions, and improvements to the model.

Mathematical Models

Whenever one seeks to analyze mathematically a problem arising in the "real" world, the first order of business is the selection of a "Mathematical model" or formulation for the problem. That is, one must choose or invent some mathematical problem to represent the real problem.

One of the fundamental models for examining the transmission of infection is SIR. A list of the three fundamental presumptions for the SIR model are listed below:

- In order for the population as a whole to remain steady, we assume that the epidemic will be short.
- Next, we make the assumption that the number of infectious agents and the population is directly correlated.
- At a steady rate, the pathogens recover or die.

SIR model

The basic SIR model's parameters are described in the section below. [1].

- Susceptible S: Part of the population who are unaffected and prone to be infected
- Infectious I: Part of the population who are already infected
- Recovered R: Part of the population who recovered from the disease
- Population N: Total population that has been considered

We investigate the following ordinary differential equations for time t and the accompanying assumptions:

$$N = N(t), S = S(t), I = I(t), R = R(t)$$

$$N = S + I + R$$

$$N(t) = N(0) \forall t$$

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$

$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

where, β is the infectious rate, I is no. of infectious, and γ S is the cure rate. Initially, $S = S_0, I = I_0, R = 0$.

Total Population remains constant,

$$\frac{ds}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0,$$

$$\frac{d(S + I + R)}{dt} = 0,$$

$$S + I + R = S_0 + I$$

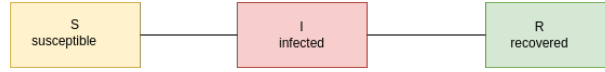


Fig 1. SIR Model

SEIR Model

The distinction between SIR and SEIR is the extra compartment exposed, denoted as E. models. By including exposed compartments to the SIR model, we can examine those who are contaminated but not yet contagious [8]. $N = S + E + I + R$ is the SEIR model's underlying principle.

1. Total population that is considered, **population N**
2. A population segment who is susceptible to infection and yet in the latency stage, **Exposed E**
3. Unaffected individuals in the population, **Susceptible S**
4. Illnesses that are contagious among some people, **Infectious I**
5. A portion of the population that beat the illness, **Recovered R**

Hence for the human population, we have

$$N(t) = S(t) + E(t) + IA(t) + IS(t) + R(t)$$



Fig 2. SEIR Model

$$\frac{dS}{dt} = -\beta SI/N$$

$$\frac{dE}{dt} = \beta SI/N - \delta E$$

$$\frac{dI}{dt} = \beta SI/N - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

Studies have shown that the virus can be transmitted in two ways, namely: human to human and environment to human. The epidemic data indicates that both asymptomatic IA (t) and asymptomatic IS (t) infected individuals spread the COVID-19 virus to susceptible persons S(t) with whom they are in close contact. In addition, when infected individuals sneeze or cough, without taking the necessary precautions, the virus spreads to the environment they are in. Since the pathogen P(t) is known to survive in the environment for some days, susceptible individuals S(t) in

close contact to this environment are likely to get exposed to these pathogens, especially in the early days of the COVID-19 outbreak before hygiene protocols are implemented. In the process of disease spread, the susceptible individual first moves to the exposed population $E(t)$ since the host has an incubation period[5]. The exposed individual moves to either an asymptomatic $IA(t)$ or symptomatic $IS(t)$ infectious population. $P(t)$ is the number or quantity of pathogens present during the interaction of human beings at time t . The majority of infectious individuals recover and move to the recovered human population $R(t)$.

Assigned Model

SEIR-P Mathematical Model

The SARS-COV-2 outbreak inspired the authors of this research to create this model. The following model was created to evaluate the virus's potential for spreading over time and the widespread social isolation that would result from the second epidemic. The majority of the research being conducted at the time was on finding many ways to calculate R_0 using the next-generation matrix method.

1. Total population that is considered, **population N**
2. A population segment who is susceptible to infection and yet in the latency stage, **Exposed E**
3. Unaffected individuals in the population, **Susceptible S**
4. Illnesses that are contagious among some people, **Infectious I**
5. A portion of the population that beat the illness, **Recovered R**

The deadly Covid-19 virus is widely recognized to spread from individual to individual and through contact with the environment. The virus is discharged into the nearby surroundings when an infected person sneezes or coughs, and doctors think it can survive there for up to five days. As a result, we take into account two interacting populations of pathogens and people, indicated by the letters $P(t)$ and $N(t)$, respectively. The susceptible population $S(t)$, the exposed population $E(t)$, the asymptomatic infected $IA(t)$, the symptomatic infected $IS(t)$, and the recovered population R are regarded as making up the total population $N(t)$ at any given time t . These can be shown in Figure 3 below,

In the above figure, b denotes the rate of the human population born in susceptible class $S(t)$.

The term $\frac{\beta_1 SP}{1+\alpha_1 P}$ and $\frac{\beta_2 S(IA+IS)}{1+\alpha_2(IA+IS)}$ reflect the rate at which susceptible individuals become infected by pathogens and through interactions with infectious asymptomatic $I(t)$ and infectious symptomatic $S(t)$.

The denominators in the above phrases take into account the following current expert recommendations on social isolation, the use of face masks to reduce contact with infectious people, and environmental transmission.

In order to simulate the dynamics of the transmission of COVID-19 while accounting for the environment and social distance, the authors in [6] proposed the integer-order differential equation shown below.

$$\begin{aligned} S'(t) &= b - \frac{\beta_1 SP}{1+\alpha_1 P} - \frac{\beta_2 S(IA+IS)}{1+\alpha_2(IA+IS)} + \psi E - \mu S \\ E'(t) &= \frac{\beta_1 SP}{1+\alpha_1 P} + \frac{\beta_2 S(IA+IS)}{1+\alpha_2(IA+IS)} - \psi E - \mu E - \omega E \end{aligned}$$

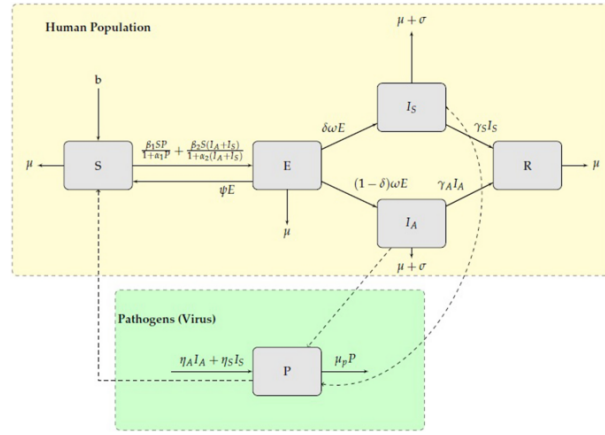


Fig 3. SEIR-P Model [1]

$$\begin{aligned}
 I_A'(t) &= (1 - \delta)\omega E - (\mu + \sigma)I_A - \gamma_A I_A \\
 I_S'(t) &= \delta\omega E - (\mu + \sigma)I_S - \gamma_S I_S \\
 R'(t) &= \gamma_S I_S + \gamma_A I_A - \mu R \\
 P'(t) &= \eta_A + \eta_S I_S - \mu_P P,
 \end{aligned}$$

considering the basic circumstances,

$$S(0) = S_0 > 0, E(0) = E_0 > 0, I_{A0} > 0, I_{S0} > 0, R(0) > 0.$$

Methods

A mathematical model of SARS-CoV-2 transmission and dissemination was developed in the study. We take into account two interdependent populations: the pathogens and the human population acting as hosts. The model separates the total number of people at time t , designated as $N(t)$, into susceptible (S), exposed (E), asymptomatic (IA), symptomatic (IS), and recovered (R) infected individuals (t). P stands for the pathogen in the environment (t). As a result, there are for the human population

$$N(t) = S(t) + E(t) + I_A(t) + I_S(t) + R(t)$$

According to studies, the virus may spread from person to person and from environment to person. The findings from the outbreak show that both asymptomatic $IA(t)$ and symptomatic $IS(t)$ infected people transmit the COVID-19 virus to susceptible individuals $S(t)$ with whom they come into contact. Also because pathogen $P(t)$ is known to remain in the environment for several days, vulnerable persons $S(t)$ in close contact with this environment are likely to be exposed to these pathogens, particularly in the early days of the COVID-19 epidemic before hygiene standards are adopted. Since the host has an incubation period, the susceptible person initially spreads the disease to the exposed population $E(t)$ [11]. The exposed person then enters an infected community that is either asymptomatic or symptomatic for $IA(t)$. $P(t)$ is the quantity or number of pathogens present at time t during human contact. The majority of infected people recover and spread to the human population that has recovered $R(t)$.

Parameter	Description
b	Birth rate of the human population
μ	Natural Human death rate
$1/\mu$	Human life expectancy
μ_p	Natural death rate of pathogens in the environment
$1/\mu_p$	Life expectancy of pathogens in the environment
α_1	Proportion of interaction with an infectious environment
α_1	Proportion of interaction with an infectious
β_1	Rate of transmission from S to E due to contact with P
β_2	Rate of transmission from S to E due to contact with I_A and/or
δ	Proportion of symptomatic infectious people
Ψ	Progression rate from E back to S due to robust immune system
ω	Progression rate from E to either I_A or I_S
σ	Death rate due to the coronavirus
γ_S	Rate of recovery of the symptomatic population
γ_A	Rate of recovery of the asymptomatic human population
η_S	Rate of virus spread to the environment by symptomatic individuals
η_A	Rate of virus spread to the environment by asymptomatic individuals

Table 1. Description of model parameters

Parameters used and justification

Following is a six-dimensional set of standard differential equations that the model ultimately leads to.

$$\begin{cases}
\frac{dS}{dt} = b - \frac{\beta_1 SP}{1+\alpha_1 P} - \frac{\beta_2 S(I_A+I_S)}{1+\alpha_2(I_A+I_S)} + \psi E - \mu S, \\
\frac{dE}{dt} = \frac{\beta_1 SP}{1+\alpha_1 P} + \frac{\beta_2 S(I_A+I_S)}{1+\alpha_2(I_A+I_S)} - \psi E - \mu E - \omega E, \\
\frac{dI_A}{dt} = (1-\delta)\omega E - (\mu + \sigma)I_A - \gamma_A I_A, \\
\frac{dI_S}{dt} = (1-\delta)\omega E - (\mu + \sigma)I_A - \gamma_A, \\
\frac{dR}{dt} = \gamma_S I_S + \gamma_A I_A + \mu R, \\
\frac{dP}{dt} = \eta_A I_A + \eta_S I_S - \mu P
\end{cases} \quad (1)$$

with the initial conditions: $S(0) > 0, E(0) > 0, I_A > 0, I_S > 0, R(0) = 0, P(0) > 0$.

The authors considered, at a rate b of individuals are born into the susceptible population. And the following parameters changed according to the model transformation.

- The parameters $\beta_1 SP$ and $\beta_2 S(I_A + I_S)$ represent the rates at which pathogens in the environment,
- $P(t)$, and infectious humans, $I_A(t)$ and $I_S(t)$, respectively, infect susceptible persons $S(t)$.

Throughout this outbreak, health professionals and governments have instructed individuals to avoid close communication with contagious people by avoiding social distancing. Over this, we propose that new infections in our model take the forms

- $\frac{\beta_1 SP}{1+\alpha_1 P}$ with interaction proportions to $_1$ and

- $\frac{\beta_2 S(I_A + I_S)}{1 + \alpha_2(I_A + I_S)}$ with interaction proportions of α_2

denoting the reciprocal of the frequency with which susceptible people contract COVID-19 from the environment and from infectious individuals, respectively.

Disease-free-equilibrium and basic reproduction number of SEIR-P model

The equilibrium points get obtained by simplifying the six-dimensional system of ordinal differential equations above when the left side is equal to zero.

Existence of disease-free-equilibrium point(DFE)

The disease-free equilibrium point and fundamental reproduction number of the model were obtained there, and numerical simulations were carried out.

In case of DFE $I_A = I_S = P = 0$ implies that $E = 0$ and $R = 0$ considering the following:

$$0 = b - \mu S \Rightarrow S = \frac{b}{\mu}$$

Thus, DFE is given by $(\frac{b}{\mu}, 0, 0, 0, 0, 0)$

The basic reproduction number

The Reproduction Number is the total number of new cases that an infected person causes in the population over the course of their whole duration of infection. We frequently discuss the basic reproduction number R_0 if this infected and infectious individual is introduced into to the totally susceptible population. The Basic Reproduction Number R_0 is the average number of subsequent infections caused by a typical instance of an infection in a community where everyone is susceptible [9]. This statistic is influenced by the frequency of contacts within the host population, the likelihood that an infection would spread through contact, and the length of the infectious period. To get the R_0 , the next-generation matrix approach is utilized.

If $x = (E, I_A, I_S, P)^T$, then the model may be expressed as

$$\frac{dx}{dt} = F(x) - V(x),$$

where

$$F(x) = \begin{pmatrix} \frac{\beta_1 SP}{1 + \alpha_1 P} + \frac{\beta_2 S(I_A + I_S)}{1 + \alpha_2(I_A + I_S)} \\ 0 \\ 0 \\ \eta_A I_A + \eta_S I_S \end{pmatrix} \text{ and}$$

$$V(x) = \begin{pmatrix} (\psi + \mu + \omega)E \\ (\mu + \sigma + \gamma_S)I_S - \delta\omega E \\ (\mu + \sigma + \gamma_A)I_A - (1 - \delta)\omega E \\ \mu_P P \end{pmatrix}$$

Then, FV^{-1} is produced by evaluating the derivatives of F and V at the previously determined disease-free equilibrium point.

$$FV^{-1} = \begin{pmatrix} \frac{\beta_2 b \delta w}{\mu C_1 C_2} + \frac{\beta_2 b (1-\delta) w}{\mu C_1 C_3} & \frac{\beta_2 b}{\mu C_2} & \frac{\beta_2 b}{\mu C_3} & \frac{\beta_1 b}{\mu \mu P} \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ \frac{\eta_S \delta w}{C_1 C_2} + \frac{\eta_A (1-\delta) w}{C_1 C_3} & \frac{\eta_S}{C_2} & \frac{\eta_A}{C_3} & 0 \end{pmatrix}$$

where

$$\begin{aligned} C_1 &= \psi + \mu + \omega, \\ C_2 &= \mu + \sigma + \gamma_S, \\ C_3 &= \mu + \sigma + \gamma_A \end{aligned}$$

The product's spectral radius, FV^{-1} , which is given by, is the reproduction number, R_0 .

$$R_0 = \frac{\frac{\beta_2 b \delta w}{\mu C_1 C_2} + \frac{\beta_2 b (1-\delta) w}{\mu C_1 C_3} + \sqrt{\left(\frac{\beta_2 b \delta w}{\mu C_1 C_2} + \frac{\beta_2 b (1-\delta) w}{\mu C_1 C_3} \right)^2 + \frac{4 \beta_2 b}{\mu \mu P} \left(\frac{\eta_S \delta w}{C_1 C_2} + \frac{\eta_A (1-\delta) w}{C_1 C_3} \right)}}{2}$$

$$R_0 = \frac{R_0^h + \sqrt{(R_0^h)^2 + 4 R_0^P}}{2}$$

Results of the given model

The authors approximated the model equations using the fourth and fifth order of Runge-Kutta methods which are implemented via *the ode45* function in MATLAB. *Note:* Here we used Julia for simulating their model.

The initial values used in the given model are,

Number of susceptible $S(0) = 93000$, exposed $E(0) = 1000$, $I_A(0) = 50$, $I_S(0) = 50$, $R(0) = 0$, $P(0) = 500$.

And the population size is given as $N = S(0) + E(0) + I_A(0) + I_S(0) + R(0) = 94100$

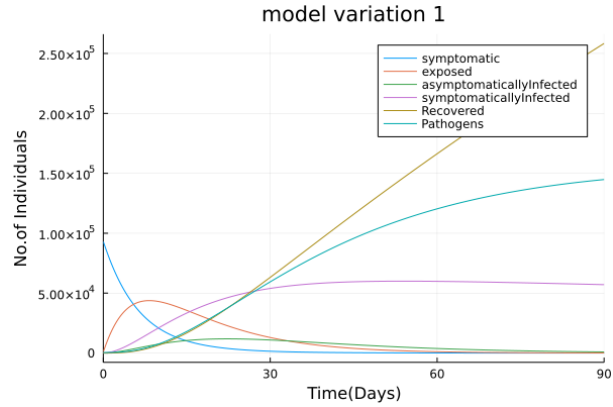


Fig 4. SEIR-P Model of COVID-19 transmission variation 1

The above figure shows the change in population as time increases from 0 to 90 days. The authors found that during the first 10 days the number of susceptible humans declines rapidly as the number of exposed individuals increased rapidly due to contact with infected individuals (I_A and I_S) and also the virus in the environment (P). After the latency period, and without mitigating the epidemic, the number of infected

individuals surges, surpassing the hospital bed capacity, set here as 8000. The infected individuals who exhibit mild or no symptoms IA are considered to be 30percent of the total infected population. The model parameters used in this simulation study are shown in Table 1. Since the symptomatic individuals IS are assumed to be more infectious than the asymptomatic IA , the transmission of COVID-19 through contacts in households, workplaces, schools, from foodstuffs, or during commute rises. This leads to a surge of the virus in environments such as workplaces, schools, foodstuffs, and public transport.

Here, In this model, we have three variations based on reproduction number. Where the constants α_1 and α_2 vary to check how frequently people get infected from the infected people or from the environment [6].

Variation 1:

The constants α_1 and α_2 in the given model represent, respectively, the reciprocals of how frequently people get COVID-19 from the environment and from other infected people.

The model demonstrates that the number of exposed, asymptomatic, and symptomatic persons increases when $\alpha_1 = 0.05$, which denotes a significant risk of contracting an infection from a contaminated environment as opposed to an afflicted individual.

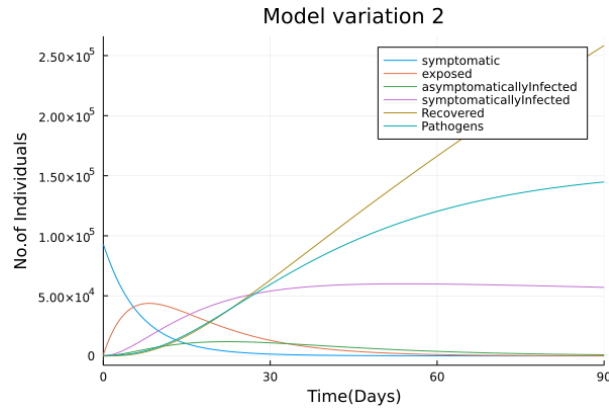


Fig 5. SEIR-P Model of COVID-19 transmission variation 2

Variation 2:

The model shows that when $\alpha_1 = 0.05$ i.e. there is a high risk of getting infected by a contaminated environment, as compared to an infected individual, the number of exposed, asymptomatic, and symptomatic individuals increases. However, when $\alpha_2 = 0.00$ which means a higher chance of getting infected by an individual, as compared to a contaminated environment.

Variation 3:

Moreover, the number of susceptible vanishes by the 23rd day for $\alpha_2 = 0.05$ since many people were infected quite rapidly, see the figure above for a duration 0 – 20 days. Therefore, with very low new infections the number of infected individuals subsequently reduces from the 25th day onward, where the number of infected individuals is seen to be lower for $\alpha_2 = 0.05$, as compared to when $\alpha_1 = 0.05$ and $\alpha_2 = 0.1$ [6].

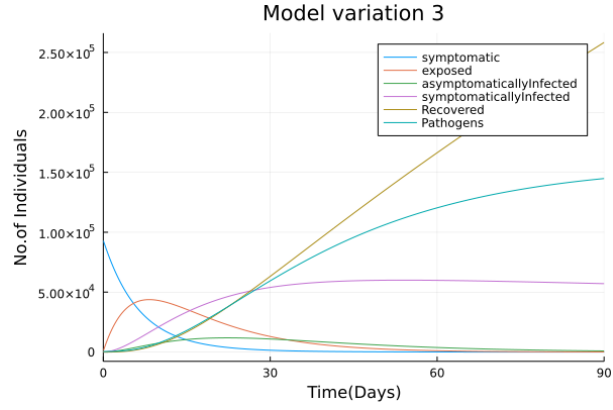


Fig 6. SEIR-P Model of COVID-19 transmission variation 3

Extended model

In the implementation, we approximated the solutions using Next-generation matrix method and solved the differential equations. Calculation of the Reproduction number took place by the same method as the core model, which is implemented using ODEProblem in Julia.

The values used in the model are from one of the Indian state called "Telangana", where the data are given as below:

total number of Population is given as $N = 350003674$,

the Susceptible $S = 2354664$,

the Exposed $E = 5000$,

Asymptomatic infected population $IA = 23700$,

Symptomatically infected population $IS = 33000$

number of Pathogens $P = 41200$,

number of Recovered $R = 0$ [12]

and parameters used are given as:

$b = 0.0569$ Birth rate of the human population in Telangana as of 2021,

$\mu = 0.18$ Natural human death rate,

$\mu_1 = 60$ Human life expectancy,

$\mu_p = 0.02$ Natural death rate of pathogens in the environment,

$\mu_p1 = 5.4$ Life expectancy of pathogens in the environment,

$\alpha_1 = 10.5$ Proportion of interaction with an infectious environment,

$\alpha_2 = 10.5$ Proportion of interaction with an infectious individual,

$\beta_1 = 8.414$ Rate of transmission from S to E due to contact with P,

$\beta_2 = 8.515$ Rate of transmission from S to E due to contact with IA and/or IS,

$\delta = 1.7$ Proportion of symptomatic infectious people,

$\psi = 0.51$ Progression rate from E back to S due to robust immune system,

$w = 0.1$ Progression rate from E to either IA or IS,

$\sigma = 0.018$ Death rate due to the coronavirus,

$\gamma_S = 3.05$ Rate of recovery of the symptomatic population,

$\gamma_A = 3.714$ Rate of recovery of the asymptomatic human population,

$\eta_S = 1.08$ Rate of virus spread to the environment by symptomatic infectious individuals,

$\eta_A = 1.09$ Rate of virus spread to the environment by asymptomatic infectious individuals [13].

The differential equations used for the implemented model,

$$S'(t) = b - \frac{\beta_1 SP}{1+\alpha_1 P} - \frac{\beta_2 S(I_A+I_S)}{1+\alpha_2(I_A+I_S)} + \psi E - \mu S$$

$$E'(t) = \frac{\beta_1 SP}{1+\alpha_1 P} + \frac{\beta_2 S(I_A+I_S)}{1+\alpha_2(I_A+I_S)} - \psi E - \mu E - \omega E ,$$

$$I_{A'}(t) = (1 - \delta)\omega E - (\mu + \sigma)I_A - \gamma_A I_A ,$$

$$I_{S'}(t) = \delta\omega E - (\mu + \sigma)I_S - \gamma_S I_S ,$$

$$R'(t) = \gamma_S I_S + \gamma_A I_A - \mu R$$

$$P'(t) = \eta_A + \eta_S I_S - \mu_P P ,$$

The reproduction number of the extended model is,

$$R_0 = \frac{\frac{\beta_2 b \delta \omega}{\mu C_1 C_2} + \frac{\beta_2 b (1-\delta) \omega}{\mu C_1 C_3} + \sqrt{\left(\frac{\beta_2 b \delta \omega}{\mu C_1 C_2} + \frac{\beta_2 b (1-\delta) \omega}{\mu C_1 C_3}\right)^2 + \frac{4 \beta_2 b}{\mu \mu_P} \left(\frac{\eta_S \delta \omega}{C_1 C_2} + \frac{\eta_A (1-\delta) \omega}{C_1 C_3}\right)}}{2}$$

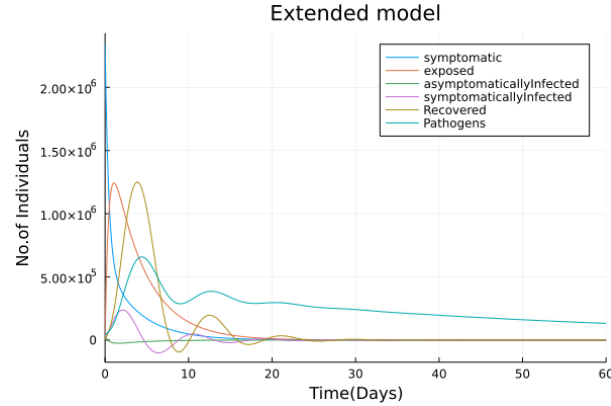


Fig 7. SEIR-P Model of COVID-19 transmission variation in Telangana

Observations: Here we can see the Infected (Asymptomatic and Symptomatic) are decreasing after 50 days. When the exposed population maintains social distancing the infection rate gradually decreases. Based on the R_0 value (0.56), we can confirm that the infection rate can be halted while following social distancing.

Discussions

An Extended SEIR-P core model is designed to identify and analyze the asymptomatic and symptomatic undetected infected cases while following social distancing. In the early days of the outbreak, there was no clear picture of the effect of social distancing but after a few days (about 20 days) the number of infected cases decreased.

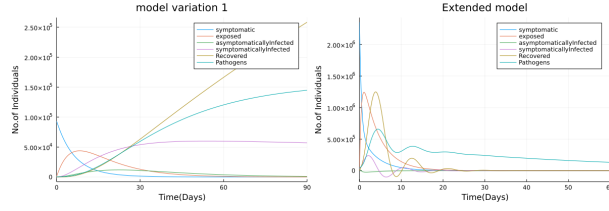


Fig 8. Comparison of models

In the given SEIR-P model, we have observed that the authors have taken into account the testing parameters α_1 and α_2 . With these parameters set high, the death rate decreased and the recovery rate increased. In the figure above, the R_0 value is affected by the two parameters. If the R_0 value is more than 1(4.49) the infection rate will increase, if the R_0 value is less than 1(0.56) the infection rate will decrease.

Hence, the implemented model clearly demonstrates how keeping social distance might lower the infection rate.

Extended model limitations

- This model is only intended to be used for a short period of time (3 months), after which the model may overestimate
- When more states or entities are incorporated into the data, the model alters

Possible extensions

We should consider the fact that people who follow social distancing may get infected and their condition can get severe. So the population should again be monitored under susceptible population. So the small improvement that can be made to this model could be the introduction of home quarantine individuals as a separate compartment.

Conclusion

In this paper, We first examined the SIR and SEIR models, then their relationship to the SEIR-P model, which formed the SEIR model's connection with Pathogens. For the dynamics of COVID-19 illness, we propose a newly implemented model where the data is used from the Indian state "Telangana" and performed the simulation and analysis. We considered that the numerical simulations aided the established characteristics of the proposed model and, more importantly, clarified the requirement for adherence to rules requiring the use of constants α_1 and α_2 preventive measures, such as social distancing, isolation of infectious and infected individuals, and frequent hand washing, in order to eradicate the deadly virus from the population.

Our findings suggest that the second outbreak in India can be halted the spread of Coronavirus by following social distancing.

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The Document's Ownwership

Communicating, coordinating, and reaching a planned conclusion all play an essential part in a group. We worked together to create a concise overview.

Tasks by Prativa Nepal

Ms. Prativa Nepal has done extensive research and acquired all of the material required to construct mathematical models and mathematical approaches, as well as documentation of the majority of the latex document.

- Deeper understanding of the Topic
- Examining several research papers, summarizing the final results
- Documentation in LATEX
- Introduction, Background, Mathematical Models, Conclusion
- Equilibrium and basic reproduction number of SEIR-P model
- Assisting in Julia code

Tasks by Shivakrishna Karnati

Mr. Shivakrishna karnati has done a lot of research and read many articles related to the scientific paper and gathered all the necessary information presented in the paper. The following are the tasks done by him

- Abstract
- Collecting data from different sources (COVID-19 data in Indian state)
- Implementation of the given model and proposed model in Julia
- Finding results of the given model and the extended model
- Limitations and possible extensions
- Assistance in Latex document
- Discussions

Tasks by Janavi Nayak

Ms. Janavi Nayak has done a lot of research and gathered the necessary information needed to calculate the reproduction number, SIR, SEIR, and SEIRP models. The following are her contributions:

- Understanding COVID models from different papers
- Collection of data from different sources like WHO, ICMR, and other websites
- Calculation of Reproduction number
- Existence of a disease-free-equilibrium point(DFE)
- Next-generation matrix
- Content collection for SIR and SEIR model

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